



1

SEQUENCE LISTING

<110> ENDOU, HITOSHI
KANAI, YOSHIKATSU

<120> NEUTRAL AMINO ACID TRANSPORTER AND GENE THEREOF

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<140> 09/786,389

<141> 2001-07-18

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<170> PatentIn Ver. 2.1

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TECH CENTER 1600/2900

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 agaaccagac cggcaccatg gggctccacc acacacctct gtccacctcc ataattcctg 2552
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 gtctgttccg gggagacggg tgagtccagc agcacatcca ctgaagcagc tgatctgact 2792
 gaaggacttg agggcatgag aatccccgc tggcccttcc attgcctcag agctggcctc 2852
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 ggcaagtctt ggtccacgtt catggtgctg acccaggccc tctgagaagg ccctgtcatt 3092
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 ctattgtatt aatgactagt ctgttacatt agactggggg tggggtgcaa gggctctgctg 3392

gtttgtgagg ctttttgatt gggggggtgg tttgtttttt ttttttaaag ctattggagt 3452

tct

3455

<210> 4

<211> 512

<212> PRT

<213> Rattus sp.

<400> 4

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Thr	Ala	Ala	Glu	Glu	Glu	Arg	Gln	Ala	Arg	Glu	Lys	Met	Leu	Glu	Ala	20	25	30	
Arg	Arg	Gly	Asp	Gly	Ala	Asp	Pro	Glu	Gly	Glu	Gly	Val	Thr	Leu	Gln	35	40	45	
Arg	Asn	Ile	Thr	Leu	Ile	Asn	Gly	Val	Ala	Ile	Ile	Val	Gly	Thr	Ile	50	55	60	
Ile	Gly	Ser	Gly	Ile	Phe	Val	Thr	Pro	Thr	Gly	Val	Leu	Lys	Glu	Ala	65	70	75	80
Gly	Ser	Pro	Gly	Leu	Ser	Leu	Val	Val	Trp	Ala	Val	Cys	Gly	Val	Phe	85	90	95	
Ser	Ile	Val	Gly	Ala	Leu	Cys	Tyr	Ala	Glu	Leu	Gly	Thr	Thr	Ile	Ser	100	105	110	
Lys	Ser	Gly	Gly	Asp	Tyr	Ala	Tyr	Met	Leu	Glu	Val	Tyr	Gly	Ser	Leu	115	120	125	
Pro	Ala	Phe	Leu	Lys	Leu	Trp	Ile	Glu	Leu	Leu	Ile	Ile	Arg	Pro	Ser	130	135	140	
Ser	Gln	Tyr	Ile	Val	Ala	Leu	Val	Phe	Ala	Thr	Tyr	Leu	Leu	Lys	Pro	145	150	155	160
Val	Phe	Pro	Thr	Cys	Pro	Val	Pro	Glu	Glu	Ala	Ala	Lys	Leu	Val	Ala	165	170	175	
Cys	Leu	Cys	Val	Leu	Leu	Leu	Thr	Ala	Val	Asn	Cys	Tyr	Ser	Val	Lys	180	185	190	
Ala	Ala	Thr	Arg	Val	Gln	Asp	Ala	Phe	Ala	Ala	Ala	Lys	Leu	Leu	Ala	195	200	205	
Leu	Ala	Leu	Ile	Ile	Leu	Leu	Gly	Phe	Ile	Gln	Met	Gly	Lys	Asp	Ile	210	215	220	
Gly	Gln	Gly	Asp	Ala	Ser	Asn	Leu	His	Gln	Lys	Leu	Ser	Phe	Glu	Gly	225	230	235	240

Thr Asn Leu Asp Val Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu
 245 250 255
 Phe Ala Tyr Gly Gly Trp Asn Tyr Leu Asn Phe Val Thr Glu Glu Met
 260 265 270
 Ile Asn Pro Tyr Arg Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro
 275 280 285
 Ile Val Thr Leu Val Tyr Val Leu Thr Asn Leu Ala Tyr Phe Thr Thr
 290 295 300
 Leu Ser Thr Asn Gln Met Leu Thr Ser Glu Ala Val Ala Val Asp Phe
 305 310 315 320
 Gly Asn Tyr His Leu Gly Val Met Ser Trp Ile Ile Pro Val Phe Val
 325 330 335
 Gly Leu Ser Cys Phe Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser
 340 345 350
 Arg Leu Phe Phe Val Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu
 355 360 365
 Ser Met Ile His Pro Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe
 370 375 380
 Thr Cys Val Met Thr Leu Met Tyr Ala Phe Ser Arg Asp Ile Phe Ser
 385 390 395 400
 Ile Ile Asn Phe Phe Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala
 405 410 415
 Ile Ile Gly Met Met Trp Leu Arg Phe Lys Lys Pro Glu Leu Glu Arg
 420 425 430
 Pro Ile Lys Val Asn Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys
 435 440 445
 Leu Phe Leu Ile Ala Val Ser Phe Trp Lys Thr Pro Leu Glu Cys Gly
 450 455 460
 Ile Gly Phe Ala Ile Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly
 465 470 475 480
 Val Trp Trp Lys Asn Lys Pro Lys Trp Ile Leu Gln Val Ile Phe Ser
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 500 505 510

<210> 5

<211> 1863

<212> DNA

<213> Homo sapiens

<220>
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 <222> (1)..(109)

<220>
 <221> CDS
 <222> (110)..(1699)

<220>
 <221> 3' UTR
 <222> (1700)..(1863)

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 Met Ser Gln
 1
 gac acc gag gtg gat atg aag gag gtg gag ctg aat gag tta gag ccc 166
 Asp Thr Glu Val Asp Met Lys Glu Val Glu Leu Asn Glu Leu Glu Pro
 5 10 15
 gag aag cag ccg atg aac gcg gcg tct ggg gcg gcc atg tcc ctg gcg 214
 Glu Lys Gln Pro Met Asn Ala Ala Ser Gly Ala Ala Met Ser Leu Ala
 20 25 30 35
 gga gcc gag aag aat ggt ctg gtg aag atc aag gtg gcg gaa gac gag 262
 Gly Ala Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala Glu Asp Glu
 40 45 50
 gcg gag gcg gca gcc gcg gct aag ttc acg ggc ctg tcc aag gag gag 310
 Ala Glu Ala Ala Ala Ala Ala Lys Phe Thr Gly Leu Ser Lys Glu Glu
 55 60 65
 ctg ctg aag gtg gca ggc agc ccc ggc tgg gta cgc acc cgc tgg gca 358
 Leu Leu Lys Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg Trp Ala
 70 75 80
 ctg ctg ctg ctc ttc tgg ctc ggc tgg ctc ggc atg ctt gct ggt gcc 406
 Leu Leu Leu Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala Gly Ala
 85 90 95
 gtg gtc ata atc gtg cga gcg ccg cgt tgt cgc gag cta ccg gcg cag 454
 Val Val Ile Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro Ala Gln
 100 105 110 115
 aag tgg tgg cac acg ggc gcc ctc tac cgc atc ggc gac ctt cag gcc 502
 Lys Trp Trp His Thr Gly Ala Leu Tyr Arg Ile Gly Asp Leu Gln Ala
 120 125 130
 ttc cag ggc cac ggc gcg ggc aac ctg gcg ggt ctg aag ggg cgt ctc 550
 Phe Gln Gly His Gly Ala Gly Asn Leu Ala Gly Leu Lys Gly Arg Leu
 135 140 145
 gat tac ctg agc tct ctg aag gtg aag ggc ctt gtg ctg ggt cca att 598
 Asp Tyr Leu Ser Ser Leu Lys Val Lys Gly Leu Val Leu Gly Pro Ile
 150 155 160

cac aag aac cag aag gat gat gtc gct cag act gac ttg ctg cag atc	646
His Lys Asn Gln Lys Asp Val Ala Gln Thr Asp Leu Leu Gln Ile	
165 170 175	
gac ccc aat ttt ggc tcc aag gaa gat ttt gac agt ctc ttg caa tcg	694
Asp Pro Asn Phe Gly Ser Lys Glu Asp Phe Asp Ser Leu Leu Gln Ser	
180 185 190 195	
gct aaa aaa aag agc atc cgt gtc att ctg gac ctt act ccc aac tac	742
Ala Lys Lys Lys Ser Ile Arg Val Ile Leu Asp Leu Thr Pro Asn Tyr	
200 205 210	
cgg ggt gag aac tcg tgg ttc tcc act cag gtt gac act gtg gcc acc	790
Arg Gly Glu Asn Ser Trp Phe Ser Thr Gln Val Asp Thr Val Ala Thr	
215 220 225	
aag gtg aag gat gct ctg gag ttt tgg ctg caa gct ggc gtg gat ggg	838
Lys Val Lys Asp Ala Leu Glu Phe Trp Leu Gln Ala Gly Val Asp Gly	
230 235 240	
ttc cag gtt cgg gac ata gag aat ctg aag gat gca tcc tca ttc ttg	886
Phe Gln Val Arg Asp Ile Glu Asn Leu Lys Asp Ala Ser Ser Phe Leu	
245 250 255	
gct gag tgg caa aat atc acc aag ggc ttc agt gaa gac agg ctc ttg	934
Ala Glu Trp Gln Asn Ile Thr Lys Gly Phe Ser Glu Asp Arg Leu Leu	
260 265 270 275	
att gcg ggg act aac tcc tcc gac ctt cag cag atc ctg agc cta ctc	982
Ile Ala Gly Thr Asn Ser Ser Asp Leu Gln Gln Ile Leu Ser Leu Leu	
280 285 290	
gaa tcc aac aaa gac ttg ctg ttg act agc tca tac ctg tct gat tct	1030
Glu Ser Asn Lys Asp Leu Leu Leu Thr Ser Ser Tyr Leu Ser Asp Ser	
295 300 305	
ggg tct act ggg gag cat aca aaa tcc cta gtc aca cag tat ttg aat	1078
Gly Ser Thr Gly Glu His Thr Lys Ser Leu Val Thr Gln Tyr Leu Asn	
310 315 320	
gcc act ggc aat cgc tgg tgc agc tgg agt ttg tct cag gca agg ctc	1126
Ala Thr Gly Asn Arg Trp Cys Ser Trp Ser Leu Ser Gln Ala Arg Leu	
325 330 335	
ctg act tcc ttc ttg ccg gct caa ctt ctc cga ctc tac cag ctg atg	1174
Leu Thr Ser Phe Leu Pro Ala Gln Leu Leu Arg Leu Tyr Gln Leu Met	
340 345 350 355	
ctc ttc acc ctg cca ggg acc cct gtt ttc agc tac ggg gat gag att	1222
Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly Asp Glu Ile	
360 365 370	
ggc ctg gat gca gct gcc ctt cct gga cag cct atg gag gct cca gtc	1270
Gly Leu Asp Ala Ala Ala Leu Pro Gly Gln Pro Met Glu Ala Pro Val	
375 380 385	

atg ctg tgg gat gag tcc agc ttc cct gac atc cca ggg gct gta agt 1318
 Met Leu Trp Asp Glu Ser Ser Phe Pro Asp Ile Pro Gly Ala Val Ser
 390 395 400

gcc aac atg act gtg aag ggc cag agt gaa gac cct ggc tcc ctc ctt 1366
 Ala Asn Met Thr Val Lys Gly Gln Ser Glu Asp Pro Gly Ser Leu Leu
 405 410 415

tcc ttg ttc cgg cgg ctg agt gac cag cgg agt aag gag cgc tcc cta 1414
 Ser Leu Phe Arg Arg Leu Ser Asp Gln Arg Ser Lys Glu Arg Ser Leu
 420 425 430 435

ctg cat ggg gac ttc cac gcg ttc tcc gct ggg cct gga ctc ttc tcc 1462
 Leu His Gly Asp Phe His Ala Phe Ser Ala Gly Pro Gly Leu Phe Ser
 440 445 450

tat atc cgc cac tgg gac cag aat gag cgt ttt ctg gta gtg ctt aac 1510
 Tyr Ile Arg His Trp Asp Gln Asn Glu Arg Phe Leu Val Val Leu Asn
 455 460 465

ttt ggg gat gtg ggc ctc tcg gct gga ctg cag gcc tcc gac ctg cct 1558
 Phe Gly Asp Val Gly Leu Ser Ala Gly Leu Gln Ala Ser Asp Leu Pro
 470 475 480

gcc agc gcc agc ctc cca gcc aag gct gac ctc ctg ctc agc acc cag 1606
 Ala Ser Ala Ser Leu Pro Ala Lys Ala Asp Leu Leu Leu Ser Thr Gln
 485 490 495

cca ggc cgt gag gag ggc tcc cct ctt gag ctg gaa cgc ctg aaa ctg 1654
 Pro Gly Arg Glu Glu Gly Ser Pro Leu Glu Leu Glu Arg Leu Lys Leu
 500 505 510 515

gag cct cac gaa ggg ctg ctg ctc cgc ttc ccc tac gcg gcc tga 1699
 Glu Pro His Glu Gly Leu Leu Leu Arg Phe Pro Tyr Ala Ala
 520 525

cttcagcctg acatggaccc actacccttc tcctttcctt ccagggccct ttggttctga 1759

tttttctctt ttttaaaaac aaacaaacaa actgttgacag attatgagtg aacccccaaa 1819

taggggtgttt tctgccttca aataaaaagtc acccctgcat ggtg 1863

<210> 6

<211> 529

<212> PRT

<213> Homo sapiens

<400> 6

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Leu Glu Pro Glu Lys Gln Pro Met Asn Ala Ala Ser Gly Ala Ala Met
 20 25 30

Ser Leu Ala Gly Ala Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala
 35 40 45

Glu	Asp	Glu	Ala	Glu	Ala	Ala	Ala	Ala	Ala	Lys	Phe	Thr	Gly	Leu	Ser	50	55	60
Lys	Glu	Glu	Leu	Leu	Lys	Val	Ala	Gly	Ser	Pro	Gly	Trp	Val	Arg	Thr	65	70	75
Arg	Trp	Ala	Leu	Leu	Leu	Leu	Phe	Trp	Leu	Gly	Trp	Leu	Gly	Met	Leu	85	90	95
Ala	Gly	Ala	Val	Val	Ile	Ile	Val	Arg	Ala	Pro	Arg	Cys	Arg	Glu	Leu	100	105	110
Pro	Ala	Gln	Lys	Trp	Trp	His	Thr	Gly	Ala	Leu	Tyr	Arg	Ile	Gly	Asp	115	120	125
Leu	Gln	Ala	Phe	Gln	Gly	His	Gly	Ala	Gly	Asn	Leu	Ala	Gly	Leu	Lys	130	135	140
Gly	Arg	Leu	Asp	Tyr	Leu	Ser	Ser	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu	145	150	155
Gly	Pro	Ile	His	Lys	Asn	Gln	Lys	Asp	Asp	Val	Ala	Gln	Thr	Asp	Leu	165	170	175
Leu	Gln	Ile	Asp	Pro	Asn	Phe	Gly	Ser	Lys	Glu	Asp	Phe	Asp	Ser	Leu	180	185	190
Leu	Gln	Ser	Ala	Lys	Lys	Lys	Ser	Ile	Arg	Val	Ile	Leu	Asp	Leu	Thr	195	200	205
Pro	Asn	Tyr	Arg	Gly	Glu	Asn	Ser	Trp	Phe	Ser	Thr	Gln	Val	Asp	Thr	210	215	220
Val	Ala	Thr	Lys	Val	Lys	Asp	Ala	Leu	Glu	Phe	Trp	Leu	Gln	Ala	Gly	225	230	235
Val	Asp	Gly	Phe	Gln	Val	Arg	Asp	Ile	Glu	Asn	Leu	Lys	Asp	Ala	Ser	245	250	255
Ser	Phe	Leu	Ala	Glu	Trp	Gln	Asn	Ile	Thr	Lys	Gly	Phe	Ser	Glu	Asp	260	265	270
Arg	Leu	Leu	Ile	Ala	Gly	Thr	Asn	Ser	Ser	Asp	Leu	Gln	Gln	Ile	Leu	275	280	285
Ser	Leu	Leu	Glu	Ser	Asn	Lys	Asp	Leu	Leu	Leu	Thr	Ser	Ser	Tyr	Leu	290	295	300
Ser	Asp	Ser	Gly	Ser	Thr	Gly	Glu	His	Thr	Lys	Ser	Leu	Val	Thr	Gln	305	310	315
Tyr	Leu	Asn	Ala	Thr	Gly	Asn	Arg	Trp	Cys	Ser	Trp	Ser	Leu	Ser	Gln	325	330	335
Ala	Arg	Leu	Leu	Thr	Ser	Phe	Leu	Pro	Ala	Gln	Leu	Leu	Arg	Leu	Tyr	340	345	350

Gln Leu Met Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly
 355 360 365
 Asp Glu Ile Gly Leu Asp Ala Ala Ala Leu Pro Gly Gln Pro Met Glu
 370 375 380
 Ala Pro Val Met Leu Trp Asp Glu Ser Ser Phe Pro Asp Ile Pro Gly
 385 390 395 400
 Ala Val Ser Ala Asn Met Thr Val Lys Gly Gln Ser Glu Asp Pro Gly
 405 410 415
 Ser Leu Leu Ser Leu Phe Arg Arg Leu Ser Asp Gln Arg Ser Lys Glu
 420 425 430
 Arg Ser Leu Leu His Gly Asp Phe His Ala Phe Ser Ala Gly Pro Gly
 435 440 445
 Leu Phe Ser Tyr Ile Arg His Trp Asp Gln Asn Glu Arg Phe Leu Val
 450 455 460
 Val Leu Asn Phe Gly Asp Val Gly Leu Ser Ala Gly Leu Gln Ala Ser
 465 470 475 480
 Asp Leu Pro Ala Ser Ala Ser Leu Pro Ala Lys Ala Asp Leu Leu Leu
 485 490 495
 Ser Thr Gln Pro Gly Arg Glu Glu Gly Ser Pro Leu Glu Leu Glu Arg
 500 505 510
 Leu Lys Leu Glu Pro His Glu Gly Leu Leu Leu Arg Phe Pro Tyr Ala
 515 520 525

Ala

<210> 7
 <211> 1797
 <212> DNA
 <213> Rattus sp.

<220>
 <221> 5' UTR
 <222> (1)..(19)
 <220>
 <221> CDS
 <222> (20)..(1603)

<220>
 <221> 3' UTR
 <222> (1604)..(1797)

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Val Glu Leu Asn Glu Leu Glu Pro Glu Lys Gln Pro Met Asn Ala Ala	
15 20 25	
gac ggg gcg gca gcc ggg gag aag aac ggt ctg gtg aag att aag gtg	148
Asp Gly Ala Ala Ala Gly Glu Lys Asn Gly Leu Val Lys Ile Lys Val	
30 35 40	
gcc gaa gac gag gcg gaa gcc ggg gtc aag ttc aca ggc tta tcc aag	196
Ala Glu Asp Glu Ala Glu Ala Gly Val Lys Phe Thr Gly Leu Ser Lys	
45 50 55	
gag gag cta ttg aag gta gct ggc agc ccg ggc tgg gtg cgc acc cgc	244
Glu Glu Leu Leu Lys Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg	
60 65 70 75	
tgg gcg ctg ctg ctg ctc ttc tgg ctc ggt tgg ctg ggt atg ctg gcg	292
Trp Ala Leu Leu Leu Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala	
80 85 90	
ggc gcc gtg gtt atc atc gtt cgg gcg cca cgc tgc cgt gag ctg ccg	340
Gly Ala Val Val Ile Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro	
95 100 105	
gta cag aga tgg tgg cac aag ggc gcc ctc tac cgc atc ggc gac ctt	388
Val Gln Arg Trp Trp His Lys Gly Ala Leu Tyr Arg Ile Gly Asp Leu	
110 115 120	
cag gcc ttc gta ggc ccg gaa gcg aga ggc ata gct ggt ctg aag aac	436
Gln Ala Phe Val Gly Pro Glu Ala Arg Gly Ile Ala Gly Leu Lys Asn	
125 130 135	
cat ctg gag tac ttg agc acc ctg aag gtg aag ggc cta gtt ttg ggc	484
His Leu Glu Tyr Leu Ser Thr Leu Lys Val Lys Gly Leu Val Leu Gly	
140 145 150 155	
cca att cac aag aac cag aag gat gaa gtc aat gaa acc gac ttg aaa	532
Pro Ile His Lys Asn Gln Lys Asp Glu Val Asn Glu Thr Asp Leu Lys	
160 165 170	
cag att gat ccc gat tta ggc tcc cag gaa gat ttt aaa gac ctt cta	580
Gln Ile Asp Pro Asp Leu Gly Ser Gln Glu Asp Phe Lys Asp Leu Leu	
175 180 185	
caa agt gcc aag aaa aag agc att cac atc att ttg gac ctc act ccc	628
Gln Ser Ala Lys Lys Lys Ser Ile His Ile Ile Leu Asp Leu Thr Pro	
190 195 200	
aac tat aag ggc cag aat gca tgg ttc ctc cct cct cag gct gac att	676
Asn Tyr Lys Gly Gln Asn Ala Trp Phe Leu Pro Pro Gln Ala Asp Ile	
205 210 215	
gta gcc acc aaa atg aag gag gct ctg agt tct tgg ttg cag gac ggt	724
Val Ala Thr Lys Met Lys Glu Ala Leu Ser Ser Trp Leu Gln Asp Gly	
220 225 230 235	

gtg gat ggg ttc caa gtt cgg gat gtg gga aag ctg gcg aat gca tcc	772
Val Asp Gly Phe Gln Val Arg Asp Val Gly Lys Leu Ala Asn Ala Ser	
240 245 250	
ttg tac ttg gct gag tgg cag aat atc acc aag aac ttc agt gag gac	820
Leu Tyr Leu Ala Glu Trp Gln Asn Ile Thr Lys Asn Phe Ser Glu Asp	
255 260 265	
agg ctt ttg att gca ggg acc gcg tcc tct gac ctg caa caa att gtc	868
Arg Leu Leu Ile Ala Gly Thr Ala Ser Ser Asp Leu Gln Gln Ile Val	
270 275 280	
aac ata ctt gaa tcc acc agc gat ctg ctg ctg acc agc tca tac ctg	916
Asn Ile Leu Glu Ser Thr Ser Asp Leu Leu Leu Thr Ser Ser Tyr Leu	
285 290 295	
tca cag ccc gtt ttc act ggg gag cat gca gaa ctc cta gtg att aag	964
Ser Gln Pro Val Phe Thr Gly Glu His Ala Glu Leu Leu Val Ile Lys	
300 305 310 315	
tat ttg aat gcc act ggc agc cgc tgg tgc agc tgg agt gtg tcg cag	1012
Tyr Leu Asn Ala Thr Gly Ser Arg Trp Cys Ser Trp Ser Val Ser Gln	
320 325 330	
gca gga ctc ctg aca tcc ttt ata ccg gct cag ttt ctc cga ctc tac	1060
Ala Gly Leu Leu Thr Ser Phe Ile Pro Ala Gln Phe Leu Arg Leu Tyr	
335 340 345	
cag ctg ctg ctc ttc act ctg cca gga act cct gtt ttc agc tat ggg	1108
Gln Leu Leu Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly	
350 355 360	
gat gag ctt ggc ctt cag gca gtt gcc ctt cct gga cag cct atg gag	1156
Asp Glu Leu Gly Leu Gln Ala Val Ala Leu Pro Gly Gln Pro Met Glu	
365 370 375	
gct cca ttc atg ctg tgg aat gag tct agc aac tcc caa acc tca agt	1204
Ala Pro Phe Met Leu Trp Asn Glu Ser Ser Asn Ser Gln Thr Ser Ser	
380 385 390 395	
cct gta agc ctc aac atg aca gtg aag ggc caa aat gaa gac ccc ggc	1252
Pro Val Ser Leu Asn Met Thr Val Lys Gly Gln Asn Glu Asp Pro Gly	
400 405 410	
tcc ctc ctc acc cag ttc cgg cga ctg agt gac ctc cgt ggt aag gag	1300
Ser Leu Leu Thr Gln Phe Arg Arg Leu Ser Asp Leu Arg Gly Lys Glu	
415 420 425	
cgc tct ctg tta cac ggt gac ttt gat gca ctg tct tcc tca tct ggg	1348
Arg Ser Leu Leu His Gly Asp Phe Asp Ala Leu Ser Ser Ser Ser Gly	
430 435 440	
ctc ttc tcc tac gtc cgc cac tgg gac cag aat gag cgt tac ctg gtg	1396
Leu Phe Ser Tyr Val Arg His Trp Asp Gln Asn Glu Arg Tyr Leu Val	
445 450 455	

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gtg ctc aac ttc cag gat gtg ggc ctg tca gcc agg gta gga gcc tcc 1444
Val Leu Asn Phe Gln Asp Val Gly Leu Ser Ala Arg Val Gly Ala Ser
460                465                470                475

aac ctc cct gct ggc ata agc ctg cca gcc agt gct aac ctt ttg ctt 1492
Asn Leu Pro Ala Gly Ile Ser Leu Pro Ala Ser Ala Asn Leu Leu Leu
480                485                490

agt act gac agc acc cgg cta agc cgt gag gag ggc acc tcc ctg agc 1540
Ser Thr Asp Ser Thr Arg Leu Ser Arg Glu Glu Gly Thr Ser Leu Ser
495                500                505

ctg gaa aac ctg agc ctg aat cct tat gag ggc ttg ttg tta cag ttc 1588
Leu Glu Asn Leu Ser Leu Asn Pro Tyr Glu Gly Leu Leu Leu Gln Phe
510                515                520

cct ttt gtg gcc tga tccctctaca cagaacctgc cacccttctt tccctctctca 1643
Pro Phe Val Ala
525

ggcctttgga attctggtct ttctctcctt attttgtttt tgttttttaa cttttgcaga 1703

ttacatatga attcttacac tgggggtttt tgttttcaaa ataaaaaaaa tcacccttaa 1763

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<210> 8
<211> 527
<212> PRT
<213> Rattus sp.

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20          25          30

Gly Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala Glu Asp Glu Ala
35          40          45

Glu Ala Gly Val Lys Phe Thr Gly Leu Ser Lys Glu Glu Leu Leu Lys
50          55          60

Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg Trp Ala Leu Leu Leu
65          70          75          80

Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala Gly Ala Val Val Ile
85          90          95

Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro Val Gln Arg Trp Trp
100         105         110

His Lys Gly Ala Leu Tyr Arg Ile Gly Asp Leu Gln Ala Phe Val Gly
115         120         125

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Pro	Glu	Ala	Arg	Gly	Ile	Ala	Gly	Leu	Lys	Asn	His	Leu	Glu	Tyr	Leu		
	130					135					140						
Ser	Thr	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu	Gly	Pro	Ile	His	Lys	Asn		
	145				150					155					160		
Gln	Lys	Asp	Glu	Val	Asn	Glu	Thr	Asp	Leu	Lys	Gln	Ile	Asp	Pro	Asp		
				165					170					175			
Leu	Gly	Ser	Gln	Glu	Asp	Phe	Lys	Asp	Leu	Leu	Gln	Ser	Ala	Lys	Lys		
			180					185					190				
Lys	Ser	Ile	His	Ile	Ile	Leu	Asp	Leu	Thr	Pro	Asn	Tyr	Lys	Gly	Gln		
		195					200					205					
Asn	Ala	Trp	Phe	Leu	Pro	Pro	Gln	Ala	Asp	Ile	Val	Ala	Thr	Lys	Met		
	210					215					220						
Lys	Glu	Ala	Leu	Ser	Ser	Trp	Leu	Gln	Asp	Gly	Val	Asp	Gly	Phe	Gln		
	225				230					235					240		
Val	Arg	Asp	Val	Gly	Lys	Leu	Ala	Asn	Ala	Ser	Leu	Tyr	Leu	Ala	Glu		
				245					250					255			
Trp	Gln	Asn	Ile	Thr	Lys	Asn	Phe	Ser	Glu	Asp	Arg	Leu	Leu	Ile	Ala		
			260					265					270				
Gly	Thr	Ala	Ser	Ser	Asp	Leu	Gln	Gln	Ile	Val	Asn	Ile	Leu	Glu	Ser		
		275					280					285					
Thr	Ser	Asp	Leu	Leu	Leu	Thr	Ser	Ser	Tyr	Leu	Ser	Gln	Pro	Val	Phe		
	290					295					300						
Thr	Gly	Glu	His	Ala	Glu	Leu	Leu	Val	Ile	Lys	Tyr	Leu	Asn	Ala	Thr		
	305				310					315					320		
Gly	Ser	Arg	Trp	Cys	Ser	Trp	Ser	Val	Ser	Gln	Ala	Gly	Leu	Leu	Thr		
				325					330					335			
Ser	Phe	Ile	Pro	Ala	Gln	Phe	Leu	Arg	Leu	Tyr	Gln	Leu	Leu	Leu	Phe		
			340					345					350				
Thr	Leu	Pro	Gly	Thr	Pro	Val	Phe	Ser	Tyr	Gly	Asp	Glu	Leu	Gly	Leu		
		355					360					365					
Gln	Ala	Val	Ala	Leu	Pro	Gly	Gln	Pro	Met	Glu	Ala	Pro	Phe	Met	Leu		
	370					375					380						
Trp	Asn	Glu	Ser	Ser	Asn	Ser	Gln	Thr	Ser	Ser	Pro	Val	Ser	Leu	Asn		
	385				390					395					400		
Met	Thr	Val	Lys	Gly	Gln	Asn	Glu	Asp	Pro	Gly	Ser	Leu	Leu	Thr	Gln		
				405					410					415			
Phe	Arg	Arg	Leu	Ser	Asp	Leu	Arg	Gly	Lys	Glu	Arg	Ser	Leu	Leu	His		
			420					425					430				

Gly Asp Phe Asp Ala Leu Ser Ser Ser Ser Gly Leu Phe Ser Tyr Val
 435 440 445
 Arg His Trp Asp Gln Asn Glu Arg Tyr Leu Val Val Leu Asn Phe Gln
 450 455 460
 Asp Val Gly Leu Ser Ala Arg Val Gly Ala Ser Asn Leu Pro Ala Gly
 465 470 475 480
 Ile Ser Leu Pro Ala Ser Ala Asn Leu Leu Leu Ser Thr Asp Ser Thr
 485 490 495
 Arg Leu Ser Arg Glu Glu Gly Thr Ser Leu Ser Leu Glu Asn Leu Ser
 500 505 510
 Leu Asn Pro Tyr Glu Gly Leu Leu Leu Gln Phe Pro Phe Val Ala
 515 520 525

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
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 synthesized primer sequence

<220>
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 <222> (1)..(22)

<400> 9
 cgaagtggac atgaaagatg tg

22

<210> 10
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
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<220>
 <221> primer_bind
 <222> (1)..(22)

<400> 10
 aaactaggcc cttcaccttc ag

22

<210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
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 <222> (1)..(22)

<400> 11
 actgctgctg ctcttctggc tcgg

24

<210> 12
 <211> 24
 <212> DNA
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<220>
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<220>
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 <222> (1)..(24)

<400> 12
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24

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<220>
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 <222> (1)..(24)

<400> 13
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24

<210> 14
 <211> 24
 <212> DNA
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<220>
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 <222> (1)..(24)

<400> 14
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24

<210> 15
<211> 24
<212> DNA
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<220>
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<220>
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<222> (1)..(24)

<400> 15
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24

<210> 16
<211> 24
<212> DNA
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<220>
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<220>
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<400> 16
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24

<210> 17
<211> 24
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<222> (1)..(24)

<400> 17
ttctcgggct ctaactcatt cagc

24

<210> 18
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 <212> DNA
 <213> Artificial Sequence

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 <222> (1)..(23)

<400> 18
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23

<210> 19
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
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<220>
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 <222> (1)..(17)

<400> 19
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17

<210> 20
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
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<220>
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 <222> (1)..(25)

<400> 20
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25

<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially

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synthesized primer sequence

<220>
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<222> (1)..(22)

<400> 21
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<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
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<220>
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<222> (1)..(21)

<400> 22
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<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(22)

<400> 23
cttggtttttc caccagaccc cg                22

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
      synthesized primer sequence

<220>
<221> primer_bind
<222> (1)..(22)

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<400> 24
tgagggatga gattcgtacc ag
22

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(23)

<400> 25
cctgggagga atcaccacc ttg
23

<210> 26
<211> 1524
<212> RNA
<213> Homo sapiens

<220>
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<222> (1)..(1524)

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<222> (592)..(594)
<223> This codon encodes a variable amino acid

<220>
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<222> (667)..(669)
<223> This codon encodes a variable amino acid

<220>
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<222> (682)..(684)
<223> This codon encodes a variable amino acid

<220>
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<222> (715)..(717)
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<400> 26
aug gcg ggu gcg ggc ccg aag cgg cgc gcg cua gcg gcg ccg gcg gcc 48
Met Ala Gly Ala Gly Pro Lys Arg Arg Ala Leu Ala Ala Pro Ala Ala
  1          5          10          15

gag gag aag gaa gag gcg cgg gag aag aug cug gcc gcc aag agc gcg 96
Glu Glu Lys Glu Glu Ala Arg Glu Lys Met Leu Ala Ala Lys Ser Ala
      20          25          30

```

gac ggc ucg gcg ccg gca ggc gag ggc gag ggc gug acc cug cag cgg	144
Asp Gly Ser Ala Pro Ala Gly Glu Gly Glu Gly Val Thr Leu Gln Arg	
35 40 45	
aac auc acg cug cuc aac ggc gug gcc auc auc gug ggg acc auu auc	192
Asn Ile Thr Leu Leu Asn Gly Val Ala Ile Ile Val Gly Thr Ile Ile	
50 55 60	
ggc ucg ggc auc uuc gug acg ccc acg ggc gug cuc aag gag gca ggc	240
Gly Ser Gly Ile Phe Val Thr Pro Thr Gly Val Leu Lys Glu Ala Gly	
65 70 75 80	
ucg ccg ggg cug gcg cug gug gug ugg gcc gcg ugc ggc guc uuc ucc	288
Ser Pro Gly Leu Ala Leu Val Val Trp Ala Ala Cys Gly Val Phe Ser	
85 90 95	
auc gug ggc gcg cuc ugc uac gcg gag cuc ggc acc acc auc ucc aaa	336
Ile Val Gly Ala Leu Cys Tyr Ala Glu Leu Gly Thr Thr Ile Ser Lys	
100 105 110	
ucg ggc ggc gac uac gcc uac aug cug gag guc uac ggc ucg cug ccc	384
Ser Gly Gly Asp Tyr Ala Tyr Met Leu Glu Val Tyr Gly Ser Leu Pro	
115 120 125	
gcc uuc cuc aag cuc ugg auc gag cug cuc auc auc cgg ccu uca ucg	432
Ala Phe Leu Lys Leu Trp Ile Glu Leu Leu Ile Ile Arg Pro Ser Ser	
130 135 140	
cag uac auc gug gcc cug guc uuc gcc acc uac cug cuc aag ccg cuc	480
Gln Tyr Ile Val Ala Leu Val Phe Ala Thr Tyr Leu Leu Lys Pro Leu	
145 150 155 160	
uuc ccc acc ugc ccg gug ccc gag gag gca gcc aag cuc gug gcc ugc	528
Phe Pro Thr Cys Pro Val Pro Glu Glu Ala Ala Lys Leu Val Ala Cys	
165 170 175	
cuc ugc gug cug cug cuc acg gcc gug aac ugc uac agc gug aag gcc	576
Leu Cys Val Leu Leu Leu Thr Ala Val Asn Cys Tyr Ser Val Lys Ala	
180 185 190	
gcc acc cgg guc cag gau gcc uuu gcc gcc gcc aag cuc cug gcc cug	624
Ala Thr Arg Val Gln Xaa Ala Phe Ala Ala Ala Lys Leu Leu Ala Leu	
195 200 205	
gcc cug auc auc cug cug ggc uuc guc cag auc ggg aag ggu gau gug	672
Ala Leu Ile Ile Leu Leu Gly Phe Val Gln Ile Gly Lys Gly Xaa Val	
210 215 220	
ucc aaU cua gau ccc aac uuc uca uuu gaa ggc acc aaa cug gau gug	720
Ser Asn Leu Xaa Pro Asn Phe Ser Phe Glu Gly Thr Lys Leu Xaa Val	
225 230 235 240	
ggg aac auu gug cug gca uua uac agc ggc cuc uuu gcc uau gga gga	768
Gly Asn Ile Val Leu Ala Leu Tyr Ser Gly Leu Phe Ala Tyr Gly Gly	
245 250 255	

ugg	aaU	uac	uug	aaU	uuc	guc	aca	gag	gaa	aug	auc	aac	ccc	uac	aga	816
Trp	Asn	Tyr	Leu	Asn	Phe	Val	Thr	Glu	Glu	Met	Ile	Asn	Pro	Tyr	Arg	
			260					265					270			
aac	cug	ccc	cug	gcc	auc	auc	auc	ucc	cug	ccc	auc	gug	acg	cug	gug	864
Asn	Leu	Pro	Leu	Ala	Ile	Ile	Ile	Ser	Leu	Pro	Ile	Val	Thr	Leu	Val	
			275					280					285			
uac	gug	cug	acc	aac	cug	gcc	uac	uuc	acc	acc	cug	ucc	acc	gag	cag	912
Tyr	Val	Leu	Thr	Asn	Leu	Ala	Tyr	Phe	Thr	Thr	Leu	Ser	Thr	Glu	Gln	
			290										300			
aug	cug	ucg	ucc	gag	gcc	gug	gcc	gug	gac	uuc	ggg	aac	uau	cac	cug	960
Met	Leu	Ser	Ser	Glu	Ala	Val	Ala	Val	Asp	Phe	Gly	Asn	Tyr	His	Leu	
					310						315				320	
ggc	guc	aug	ucc	ugg	auc	auc	ccc	guc	uuc	gug	ggc	cug	ucc	ugc	uuc	1008
Gly	Val	Met	Ser	Trp	Ile	Ile	Pro	Val	Phe	Val	Gly	Leu	Ser	Cys	Phe	
					325					330					335	
ggc	ucc	guc	aaU	ggg	ucc	cug	uuc	aca	ucc	ucc	agg	cuc	uuc	uuc	gug	1056
Gly	Ser	Val	Asn	Gly	Ser	Leu	Phe	Thr	Ser	Ser	Arg	Leu	Phe	Phe	Val	
					340						345				350	
ggg	ucc	cgg	gaa	ggc	cac	cug	ccc	ucc	auc	cuc	ucc	aug	auc	cac	cca	1104
Gly	Ser	Arg	Glu	Gly	His	Leu	Pro	Ser	Ile	Leu	Ser	Met	Ile	His	Pro	
					355										365	
cag	cuc	cuc	acc	ccc	gug	ccg	ucc	cuc	gug	uuc	acg	ugu	gug	aug	acg	1152
Gln	Leu	Leu	Thr	Pro	Val	Pro	Ser	Leu	Val	Phe	Thr	Cys	Val	Met	Thr	
					370										380	
cug	cuc	uac	gcc	uuc	ucc	aag	gac	auc	uuc	ucc	guc	auc	aac	uuc	uuc	1200
Leu	Leu	Tyr	Ala	Phe	Ser	Lys	Asp	Ile	Phe	Ser	Val	Ile	Asn	Phe	Phe	
						390					395				400	
agc	uuc	uuc	aac	ugg	cuc	ugc	gug	gcc	cug	gcc	auc	auc	ggc	aug	auc	1248
Ser	Phe	Phe	Asn	Trp	Leu	Cys	Val	Ala	Leu	Ala	Ile	Ile	Gly	Met	Ile	
					405					410					415	
ugg	cug	cgc	cac	aga	aag	ccu	gag	cuu	gag	cgg	ccc	auc	aag	gug	aac	1296
Trp	Leu	Arg	His	Arg	Lys	Pro	Glu	Leu	Glu	Arg	Pro	Ile	Lys	Val	Asn	
					420					425					430	
cug	gcc	cug	ccu	gug	uuc	uuc	auc	cug	gcc	ugc	cuc	uuc	cug	auc	gcc	1344
Leu	Ala	Leu	Pro	Val	Phe	Phe	Ile	Leu	Ala	Cys	Leu	Phe	Leu	Ile	Ala	
					435										445	
guc	ucc	uuc	ugg	aag	aca	ccc	gug	gag	ugu	ggc	auc	ggc	uuc	acc	auc	1392
Val	Ser	Phe	Trp	Lys	Thr	Pro	Val	Glu	Cys	Gly	Ile	Gly	Phe	Thr	Ile	
						455									460	
auc	cuc	agc	ggg	cug	ccc	guc	uac	uuc	uuc	ggg	guc	ugg	ugg	aaa	aac	1440
Ile	Leu	Ser	Gly	Leu	Pro	Val	Tyr	Phe	Phe	Gly	Val	Trp	Trp	Lys	Asn	
						470					475				480	

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aag ccc aag ugg cuc cuc cag ggc auc uuc ucc acg acc guc cug ugu 1488
Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu Cys
              485                      490                      495

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cag aag cuc aug cag gug guc ccc cag gag aca uag 1524
Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr
              500                      505

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<210> 27
<211> 1590
<212> RNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(1590)

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<220>
<221> modified_base
<222> (22)..(24)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (442)..(444)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (505)..(507)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (508)..(510)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (520)..(522)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (562)..(564)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (622)..(624)
<223> This codon encodes a variable amino acid

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<220>
<221> modified_base
<222> (658)..(660)
<223> This codon encodes a variable amino acid

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<220>
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<222> (670)..(672)
<223> This codon encodes a variable amino acid

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<222> (691)..(693)
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<222> (835)..(837)
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<223> This codon encodes a variable amino acid

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<222> (916)..(918)
<223> This codon encodes a variable amino acid

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<222> (928)..(930)
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<223> This codon encodes a variable amino acid

<220>
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<223> This codon encodes a variable amino acid

<220>

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<222> (1171)..(1173)

<223> This codon encodes a variable amino acid

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<222> (1219)..(1221)

<223> This codon encodes a variable amino acid

<220>

<221> modified_base

<222> (1408)..(1410)

<223> This codon encodes a variable amino acid

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Met	Ser	Gln	Asp	Thr	Glu	Val	Xaa	Met	Lys	Glu	Val	Glu	Leu	Asn	Glu	
1				5				10					15			

uua	gag	ccc	gag	aag	cag	ccg	aug	aac	gcg	gcg	ucu	ggg	gcg	gcc	aug	96
Leu	Glu	Pro	Glu	Lys	Gln	Pro	Met	Asn	Ala	Ala	Ser	Gly	Ala	Ala	Met	
			20					25					30			

ucc	cug	gcg	gga	gcc	gag	aag	aaU	ggU	cug	gug	aag	auc	aag	gug	gcg	144
Ser	Leu	Ala	Gly	Ala	Glu	Lys	Asn	Gly	Leu	Val	Lys	Ile	Lys	Val	Ala	
		35					40					45				

gaa	gac	gag	gcg	gag	gcg	gca	gcc	gcg	gcu	aag	uuc	acg	ggc	cug	ucc	192
Glu	Asp	Glu	Ala	Glu	Ala	Ala	Ala	Ala	Ala	Lys	Phe	Thr	Gly	Leu	Ser	
	50					55					60					

aag	gag	gag	cug	cug	aag	gug	gca	ggc	agc	ccc	ggc	ugg	gua	cgc	acc	240
Lys	Glu	Glu	Leu	Leu	Lys	Val	Ala	Gly	Ser	Pro	Gly	Trp	Val	Arg	Thr	
65					70				75						80	

cgc	ugg	gca	cug	cug	cug	cuc	uuc	ugg	cuc	ggc	ugg	cuc	ggc	aug	cuu	288
Arg	Trp	Ala	Leu	Leu	Leu	Leu	Phe	Trp	Leu	Gly	Trp	Leu	Gly	Met	Leu	
			85					90						95		

gcu	ggU	gcc	gug	guc	aua	auc	gug	cga	gcg	ccg	cgu	ugu	cgc	gag	cua	336
Ala	Gly	Ala	Val	Val	Ile	Ile	Val	Arg	Ala	Pro	Arg	Cys	Arg	Glu	Leu	
			100					105					110			

ccg	gcg	cag	aag	ugg	ugg	cac	acg	ggc	gcc	cuc	uac	cgc	auc	ggc	gac	384
Pro	Ala	Gln	Lys	Trp	Trp	His	Thr	Gly	Ala	Leu	Tyr	Arg	Ile	Gly	Asp	
		115					120					125				

cuu	cag	gcc	uuc	cag	ggc	cac	ggc	gcg	ggc	aac	cug	gcg	ggU	cug	aag	432
Leu	Gln	Ala	Phe	Gln	Gly	His	Gly	Ala	Gly	Asn	Leu	Ala	Gly	Leu	Lys	
		130				135					140					

ggg	cgu	cuc	gau	uac	cug	agc	ucu	cug	aag	gug	aag	ggc	cuu	gug	cug	480
Gly	Arg	Leu	Xaa	Tyr	Leu	Ser	Ser	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu	
145					150					155					160	

ggg cca auu cac aag aac cag aag gau gau guc gcu cag acu gac uug	528
Gly Pro Ile His Lys Asn Gln Lys Xaa Xaa Val Ala Gln Xaa Asp Leu	
165 170 175	
cug cag auc gac ccc aaU uuU ggc ucc aag gaa gau uuU gac agu cuc	576
Leu Gln Ile Asp Pro Asn Phe Gly Ser Lys Glu Xaa Phe Asp Ser Leu	
180 185 190	
uug caa ucg gcu aaa aaa aag agc auc cgu guc auu cug gac cuu acu	624
Leu Gln Ser Ala Lys Lys Lys Ser Ile Arg Val Ile Leu Asp Leu Xaa	
195 200 205	
ccc aac uac cgg ggu gag aac ucg ugg uuc ucc acu cag guu gac acu	672
Pro Asn Tyr Arg Gly Glu Asn Ser Trp Phe Ser Xaa Gln Val Asp Xaa	
210 215 220	
gug gcc acc aag gug aag gau gcu cug gag uuU ugg cug caa gcu ggc	720
Val Ala Thr Lys Val Lys Xaa Ala Leu Glu Phe Trp Leu Gln Ala Gly	
225 230 235 240	
gug gau ggg uuc cag guu cgg gac aua gag aaU cug aag gau gca ucc	768
Val Xaa Gly Phe Gln Val Arg Asp Ile Glu Asn Leu Lys Xaa Ala Ser	
245 250 255	
uca uuc uug gcu gag ugg caa aaU auc acc aag ggc uuc agu gaa gac	816
Ser Phe Leu Ala Glu Trp Gln Asn Ile Thr Lys Gly Phe Ser Glu Asp	
260 265 270	
agg cuc uug auu gcg ggg acu aac ucc ucc gac cuu cag cag auc cug	864
Arg Leu Leu Ile Ala Gly Xaa Asn Ser Ser Asp Leu Gln Gln Ile Leu	
275 280 285	
agc cua cuc gaa ucc aac aaa gac uug cug uuG acu agc uca uac cug	912
Ser Leu Leu Glu Ser Asn Lys Asp Leu Leu Leu Xaa Ser Ser Tyr Leu	
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ucu gau ucu ggu ucu acu ggg gag cau aca aaa ucc cua guc aca cag	960
Ser Xaa Ser Gly Ser Xaa Gly Glu His Thr Lys Ser Leu Val Thr Gln	
305 310 315 320	
uau uug aaU gcc acu ggc aaU cgc ugg ugc agc ugg agu uuG ucu cag	1008
Tyr Leu Asn Ala Xaa Gly Asn Arg Trp Cys Ser Trp Ser Leu Ser Gln	
325 330 335	
gca agg cuc cug acu ucc uuc uug ccg gcu caa cuu cuc cga cuc uac	1056
Ala Arg Leu Leu Xaa Ser Phe Leu Pro Ala Gln Leu Leu Arg Leu Tyr	
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cag cug aug cuc uuc acc cug cca ggg acc ccu guu uuC agc uac ggg	1104
Gln Leu Met Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly	
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gau gag auu ggc cug gau gca gcu gcc cuu ccu gga cag ccu aug gag	1152
Xaa Glu Ile Gly Leu Xaa Ala Ala Ala Leu Pro Gly Gln Pro Met Glu	
370 375 380	

gcu cca guc aug cug ugg gau gag ucc agc uuc ccu gac auc cca ggg	1200
Ala Pro Val Met Leu Trp Xaa Glu Ser Ser Phe Pro Asp Ile Pro Gly	
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gcu gua agu gcc aac aug acu gug aag ggc cag agu gaa gac ccu ggc	1248
Ala Val Ser Ala Asn Met Xaa Val Lys Gly Gln Ser Glu Asp Pro Gly	
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ucc cuc cuu ucc uug uuc cgg cgg cug agu gac cag cgg agu aag gag	1296
Ser Leu Leu Ser Leu Phe Arg Arg Leu Ser Asp Gln Arg Ser Lys Glu	
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cgc ucc cua cug cau ggg gac uuc cac gcg uuc ucc gcu ggg ccu gga	1344
Arg Ser Leu Leu His Gly Asp Phe His Ala Phe Ser Ala Gly Pro Gly	
435 440 445	
cuc uuc ucc uau auc cgc cac ugg gac cag aaU gag cgu uuu cug gua	1392
Leu Phe Ser Tyr Ile Arg His Trp Asp Gln Asn Glu Arg Phe Leu Val	
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gug cuu aac uuu ggg gau gug ggc cuc ucg gcU gga cug cag gcc ucc	1440
Val Leu Asn Phe Gly Xaa Val Gly Leu Ser Ala Gly Leu Gln Ala Ser	
465 470 475 480	
gac cug ccu gcc agc gcc agc cuc cca gcc aag gcU gac cuc cug cuc	1488
Asp Leu Pro Ala Ser Ala Ser Leu Pro Ala Lys Ala Asp Leu Leu Leu	
485 490 495	
agc acc cag cca ggc cgu gag gag ggc ucc ccu cuu gag cug gaa cgc	1536
Ser Thr Gln Pro Gly Arg Glu Glu Gly Ser Pro Leu Glu Leu Glu Arg	
500 505 510	
cug aaa cug gag ccu cac gaa ggg cug cug cuc cgc uuc ccc uac gcg	1584
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Asp	Gly	Ser	Ala	Pro	Ala	Gly	Glu	Gly	Glu	Gly	Val	Thr	Leu	Gln	Arg	35	40	45	
Asn	Ile	Thr	Leu	Leu	Asn	Gly	Val	Ala	Ile	Ile	Val	Gly	Thr	Ile	Ile	50	55	60	
Gly	Ser	Gly	Ile	Phe	Val	Thr	Pro	Thr	Gly	Val	Leu	Lys	Glu	Ala	Gly	65	70	75	80
Ser	Pro	Gly	Leu	Ala	Leu	Val	Val	Trp	Ala	Ala	Cys	Gly	Val	Phe	Ser	85	90	95	
Ile	Val	Gly	Ala	Leu	Cys	Tyr	Ala	Glu	Leu	Gly	Thr	Thr	Ile	Ser	Lys	100	105	110	
Ser	Gly	Gly	Asp	Tyr	Ala	Tyr	Met	Leu	Glu	Val	Tyr	Gly	Ser	Leu	Pro	115	120	125	
Ala	Phe	Leu	Lys	Leu	Trp	Ile	Glu	Leu	Leu	Ile	Ile	Arg	Pro	Ser	Ser	130	135	140	
Gln	Tyr	Ile	Val	Ala	Leu	Val	Phe	Ala	Thr	Tyr	Leu	Leu	Lys	Pro	Leu	145	150	155	160
Phe	Pro	Thr	Cys	Pro	Val	Pro	Glu	Glu	Ala	Ala	Lys	Leu	Val	Ala	Cys	165	170	175	
Leu	Cys	Val	Leu	Leu	Leu	Thr	Ala	Val	Asn	Cys	Tyr	Ser	Val	Lys	Ala	180	185	190	
Ala	Thr	Arg	Val	Gln	Xaa	Ala	Phe	Ala	Ala	Ala	Lys	Leu	Leu	Ala	Leu	195	200	205	
Ala	Leu	Ile	Ile	Leu	Leu	Gly	Phe	Val	Gln	Ile	Gly	Lys	Gly	Xaa	Val	210	215	220	
Ser	Asn	Leu	Xaa	Pro	Asn	Phe	Ser	Phe	Glu	Gly	Thr	Lys	Leu	Xaa	Val	225	230	235	240
Gly	Asn	Ile	Val	Leu	Ala	Leu	Tyr	Ser	Gly	Leu	Phe	Ala	Tyr	Gly	Gly	245	250	255	
Trp	Asn	Tyr	Leu	Asn	Phe	Val	Thr	Glu	Glu	Met	Ile	Asn	Pro	Tyr	Arg	260	265	270	

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Asn Leu Pro Leu Ala Ile Ile Ile Ser Leu Pro Ile Val Thr Leu Val
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Met Leu Ser Ser Glu Ala Val Ala Val Asp Phe Gly Asn Tyr His Leu
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Gly Val Met Ser Trp Ile Ile Pro Val Phe Val Gly Leu Ser Cys Phe
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Gly Ser Val Asn Gly Ser Leu Phe Thr Ser Ser Arg Leu Phe Phe Val
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Gly Ser Arg Glu Gly His Leu Pro Ser Ile Leu Ser Met Ile His Pro
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Gln Leu Leu Thr Pro Val Pro Ser Leu Val Phe Thr Cys Val Met Thr
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Leu Leu Tyr Ala Phe Ser Lys Asp Ile Phe Ser Val Ile Asn Phe Phe
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Ser Phe Phe Asn Trp Leu Cys Val Ala Leu Ala Ile Ile Gly Met Ile
                405                               410                415

Trp Leu Arg His Arg Lys Pro Glu Leu Glu Arg Pro Ile Lys Val Asn
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Leu Ala Leu Pro Val Phe Phe Ile Leu Ala Cys Leu Phe Leu Ile Ala
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Val Ser Phe Trp Lys Thr Pro Val Glu Cys Gly Ile Gly Phe Thr Ile
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Ile Leu Ser Gly Leu Pro Val Tyr Phe Phe Gly Val Trp Trp Lys Asn
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Lys Pro Lys Trp Leu Leu Gln Gly Ile Phe Ser Thr Thr Val Leu Cys
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Gln Lys Leu Met Gln Val Val Pro Gln Glu Thr
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20 25 30

Ser Leu Ala Gly Ala Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala
35 40 45

Glu	Asp	Glu	Ala	Glu	Ala	Ala	Ala	Ala	Ala	Lys	Phe	Thr	Gly	Leu	Ser	50	55	60
Lys	Glu	Glu	Leu	Leu	Lys	Val	Ala	Gly	Ser	Pro	Gly	Trp	Val	Arg	Thr	65	70	75
Arg	Trp	Ala	Leu	Leu	Leu	Leu	Phe	Trp	Leu	Gly	Trp	Leu	Gly	Met	Leu	85	90	95
Ala	Gly	Ala	Val	Val	Ile	Ile	Val	Arg	Ala	Pro	Arg	Cys	Arg	Glu	Leu	100	105	110
Pro	Ala	Gln	Lys	Trp	Trp	His	Thr	Gly	Ala	Leu	Tyr	Arg	Ile	Gly	Asp	115	120	125
Leu	Gln	Ala	Phe	Gln	Gly	His	Gly	Ala	Gly	Asn	Leu	Ala	Gly	Leu	Lys	130	135	140
Gly	Arg	Leu	Xaa	Tyr	Leu	Ser	Ser	Leu	Lys	Val	Lys	Gly	Leu	Val	Leu	145	150	155
Gly	Pro	Ile	His	Lys	Asn	Gln	Lys	Xaa	Xaa	Val	Ala	Gln	Xaa	Asp	Leu	165	170	175
Leu	Gln	Ile	Asp	Pro	Asn	Phe	Gly	Ser	Lys	Glu	Xaa	Phe	Asp	Ser	Leu	180	185	190
Leu	Gln	Ser	Ala	Lys	Lys	Lys	Ser	Ile	Arg	Val	Ile	Leu	Asp	Leu	Xaa	195	200	205
Pro	Asn	Tyr	Arg	Gly	Glu	Asn	Ser	Trp	Phe	Ser	Xaa	Gln	Val	Asp	Xaa	210	215	220
Val	Ala	Thr	Lys	Val	Lys	Xaa	Ala	Leu	Glu	Phe	Trp	Leu	Gln	Ala	Gly	225	230	235
Val	Xaa	Gly	Phe	Gln	Val	Arg	Asp	Ile	Glu	Asn	Leu	Lys	Xaa	Ala	Ser	245	250	255
Ser	Phe	Leu	Ala	Glu	Trp	Gln	Asn	Ile	Thr	Lys	Gly	Phe	Ser	Glu	Asp	260	265	270
Arg	Leu	Leu	Ile	Ala	Gly	Xaa	Asn	Ser	Ser	Asp	Leu	Gln	Gln	Ile	Leu	275	280	285
Ser	Leu	Leu	Glu	Ser	Asn	Lys	Asp	Leu	Leu	Leu	Xaa	Ser	Ser	Tyr	Leu	290	295	300
Ser	Xaa	Ser	Gly	Ser	Xaa	Gly	Glu	His	Thr	Lys	Ser	Leu	Val	Thr	Gln	305	310	315
Tyr	Leu	Asn	Ala	Xaa	Gly	Asn	Arg	Trp	Cys	Ser	Trp	Ser	Leu	Ser	Gln	325	330	335
Ala	Arg	Leu	Leu	Xaa	Ser	Phe	Leu	Pro	Ala	Gln	Leu	Leu	Arg	Leu	Tyr	340	345	350

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Ala	Pro	Val	Met	Leu	Trp	Xaa	Glu	Ser	Ser	Phe	Pro	Asp	Ile	Pro	Gly
385					390					395					400
Ala	Val	Ser	Ala	Asn	Met	Xaa	Val	Lys	Gly	Gln	Ser	Glu	Asp	Pro	Gly
				405					410						415
Ser	Leu	Leu	Ser	Leu	Phe	Arg	Arg	Leu	Ser	Asp	Gln	Arg	Ser	Lys	Glu
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Leu	Phe	Ser	Tyr	Ile	Arg	His	Trp	Asp	Gln	Asn	Glu	Arg	Phe	Leu	Val
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Val	Leu	Asn	Phe	Gly	Xaa	Val	Gly	Leu	Ser	Ala	Gly	Leu	Gln	Ala	Ser
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Asp	Leu	Pro	Ala	Ser	Ala	Ser	Leu	Pro	Ala	Lys	Ala	Asp	Leu	Leu	Leu
				485					490					495	
Ser	Thr	Gln	Pro	Gly	Arg	Glu	Glu	Gly	Ser	Pro	Leu	Glu	Leu	Glu	Arg
			500					505							
Leu	Lys	Leu	Glu	Pro	His	Glu	Gly	Leu	Leu	Leu	Arg	Phe	Pro	Tyr	Ala
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Ala